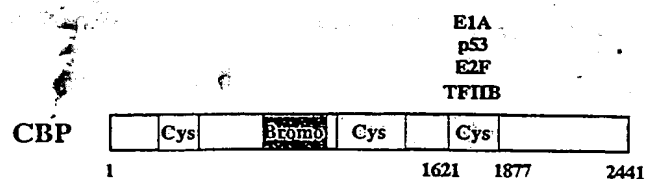


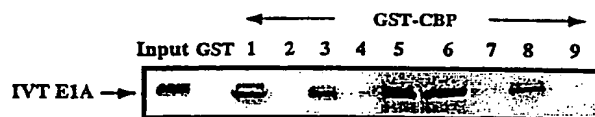
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a



b

CBP Construct	E1A Binding
1 (1715-1852)	+
2 (1715-1764)	-
3 (1765-1852)	+
4 (1765-1808)	-
5 (1808-1852)	+
6 (1808-1833)	+
7 (1835-1852)	-
8 (1808-1826)	+
9 (1808-1819)	-



c

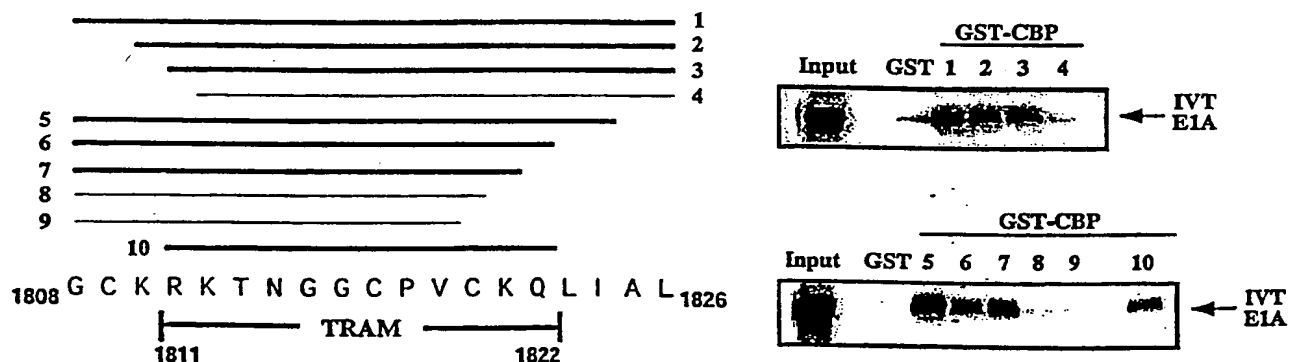


Figure 1

d

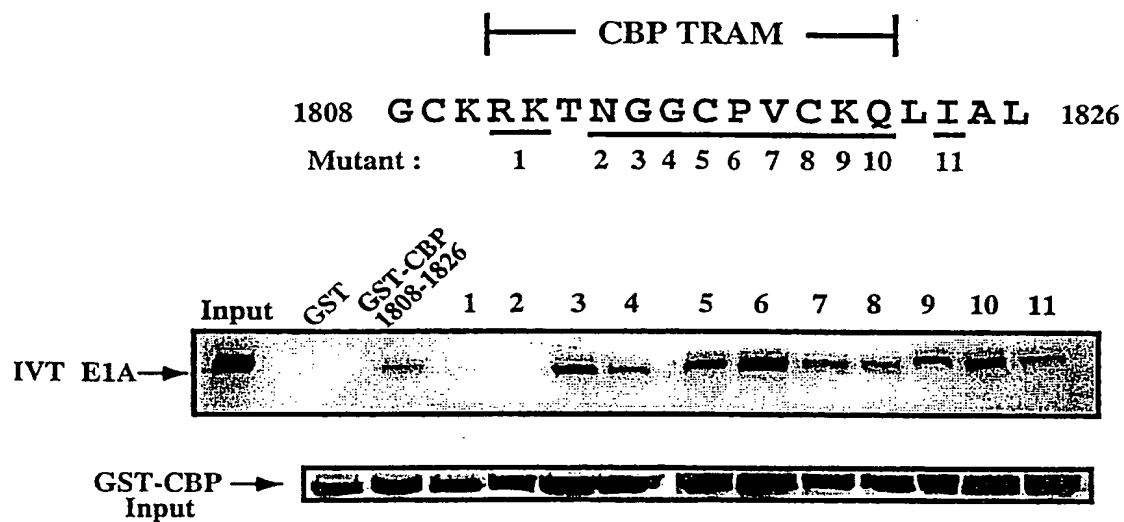
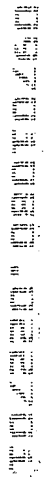


Figure 1

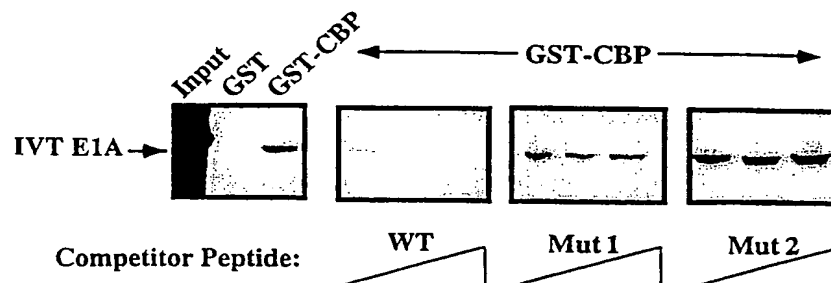


SUBSTITUTE SHEET (RULE 26)

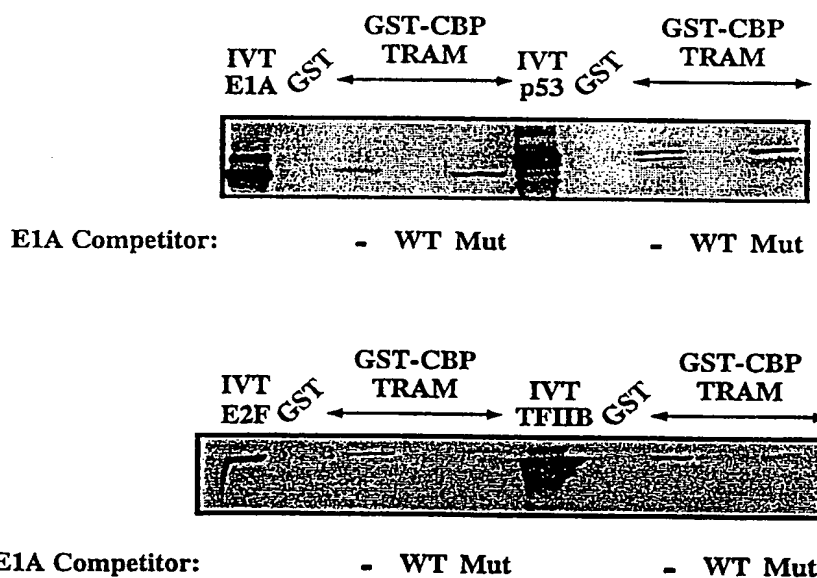
b

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Peptides: WT : V N E F F P E S L I L L
 Mut 1 : V N E F F P A S A I L L
 Mut 2 : V N E F A P A S A I A



c



d

TRAM	E1A	V N E F <u>F P E S L I L</u> A A
Interaction	p53	S Q E T <u>F S D L W K L</u> L P
Motif	E2F	F D C D <u>F G D L T P L</u> D F

Consensus: F X $\frac{E}{D}$ X X X L

Figure 2

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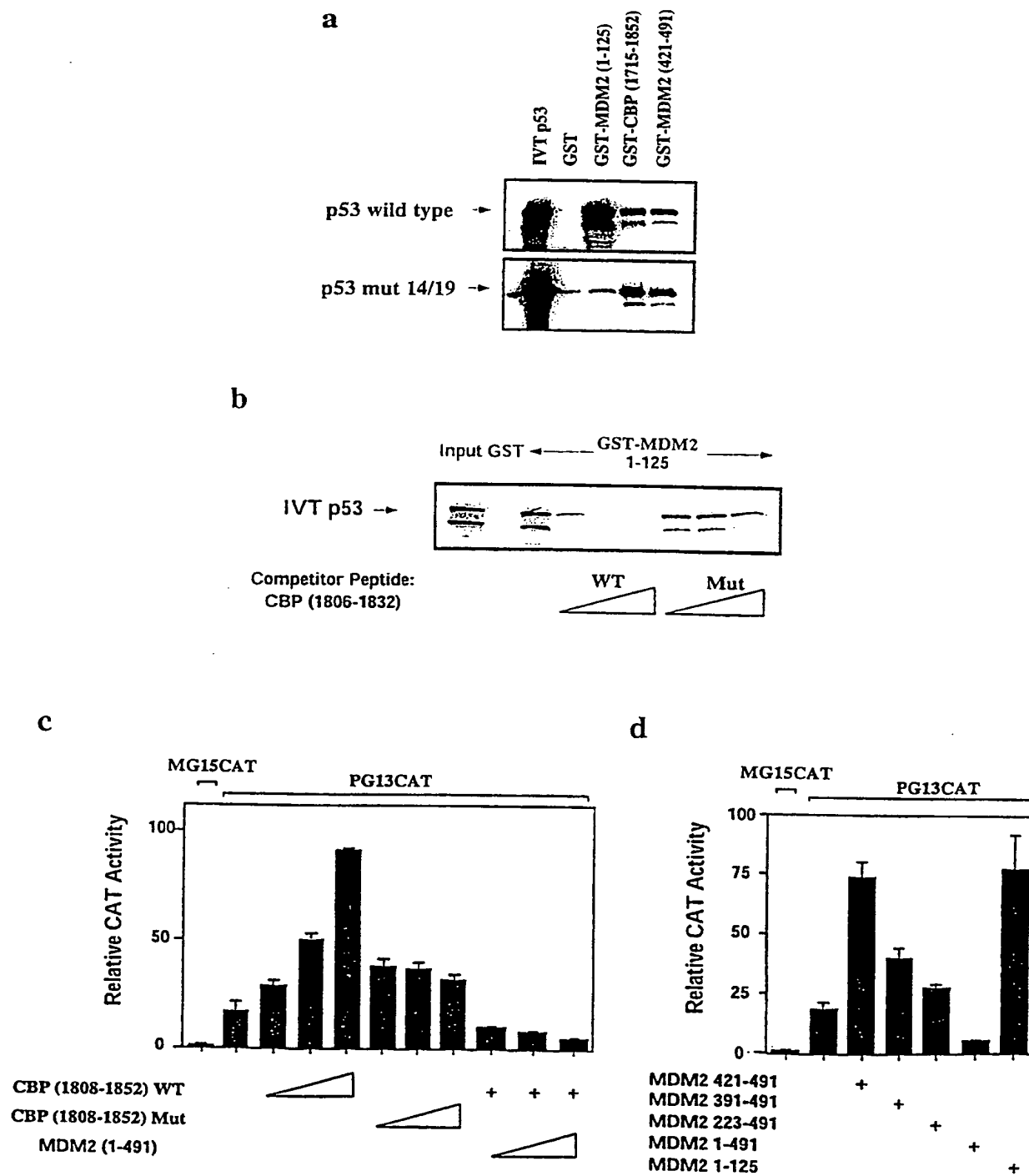
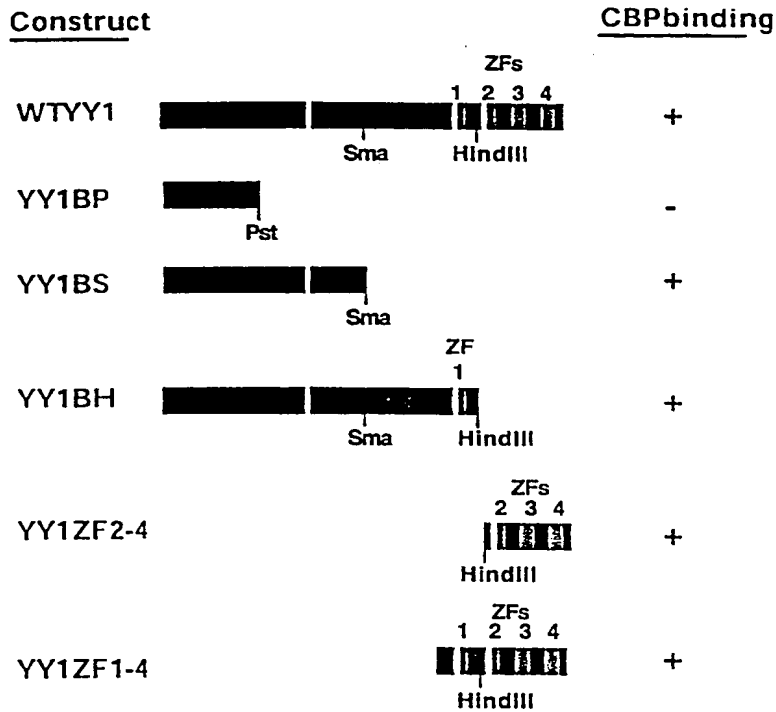
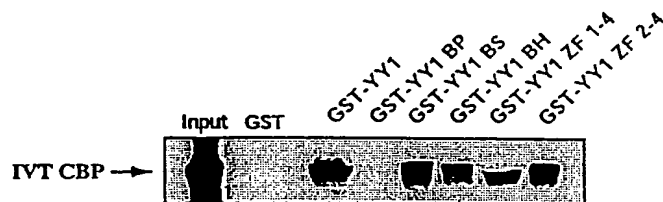


Figure 4

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b



c

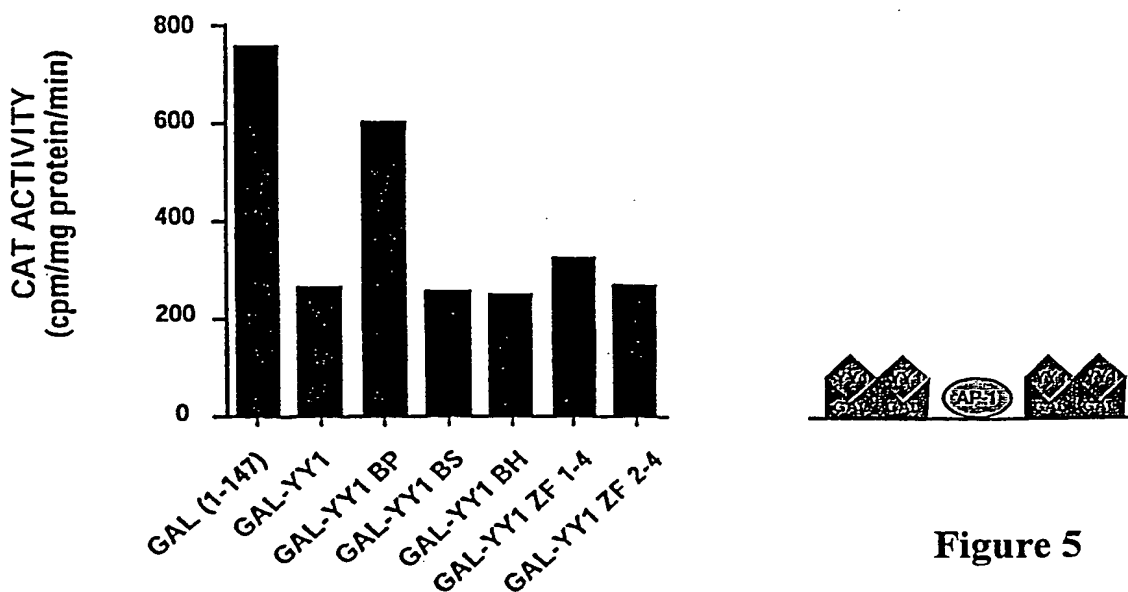


Figure 5

TRIMs	8/15	
	E1A	VNEFF <u>PESLILAA</u>
	p53	SQET <u>FSDLWKLLP</u>
	E2F	FDCDF <u>GDLTPLDF</u>
	TFIIIB	MMNA <u>FKEITTMAD</u>
	YY1	AEDG <u>FEDQILIPV</u>
	YY1	CTKM <u>FRDNSAMRK</u>
	YY1	CGKA <u>FVESSKLKR</u>
	MyoD	TTDD <u>FYDDPCFDS</u>

b

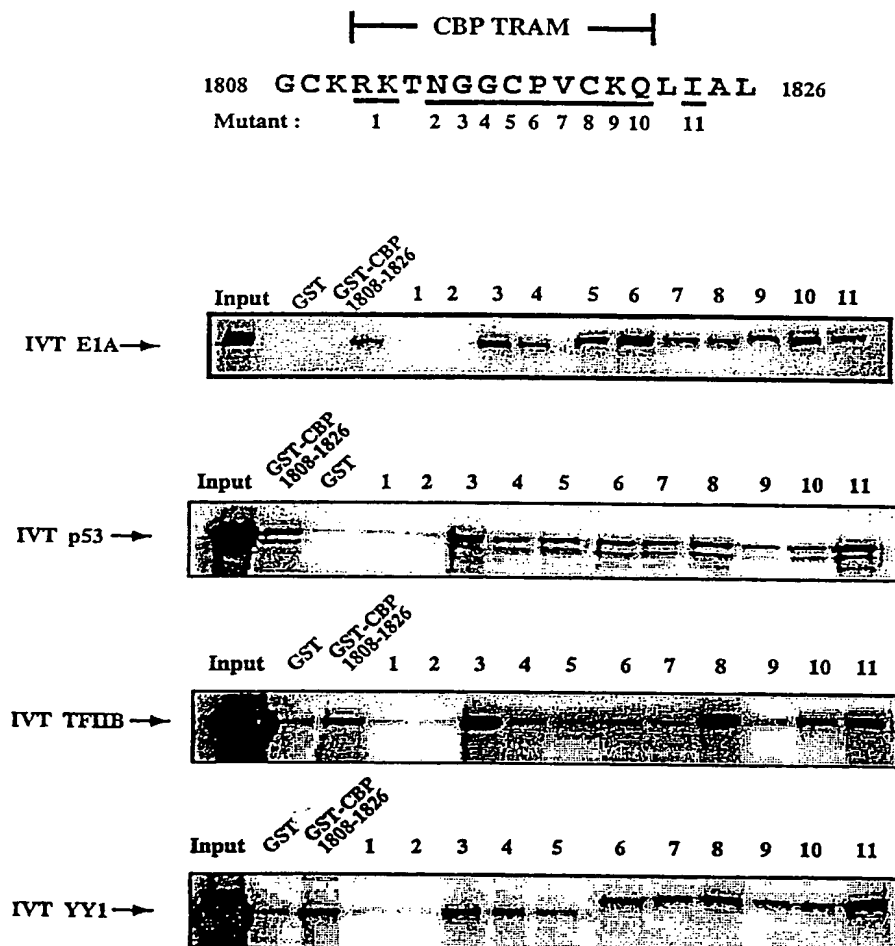


Figure 6

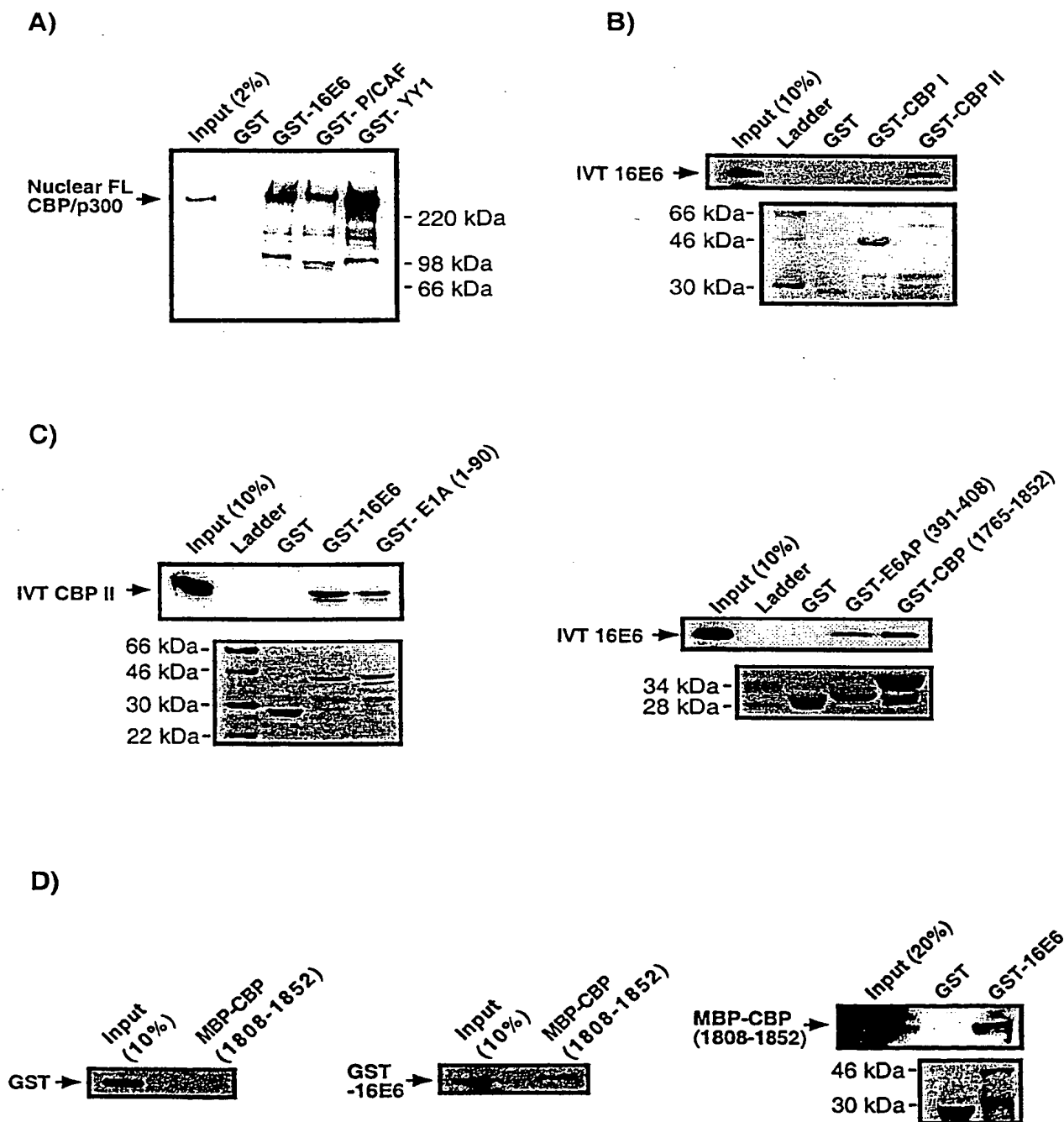
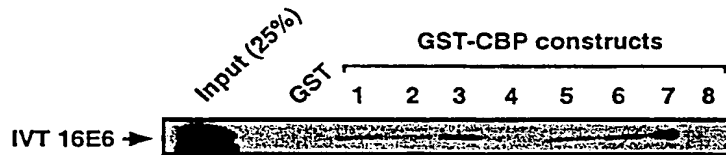
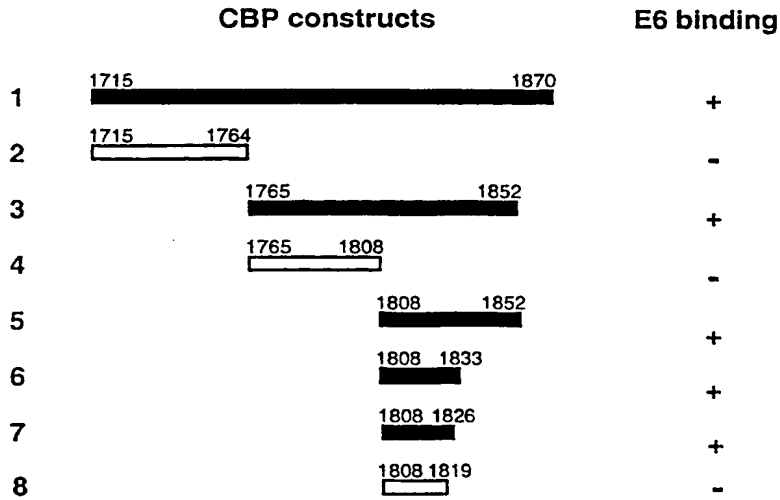


Figure 7



CBP (1808-1826): GCKRKTNGGCPVCKQLIAL
 p300 (1770-1788): GCKRKTNGGCPICKQLIAL
 *****+*****

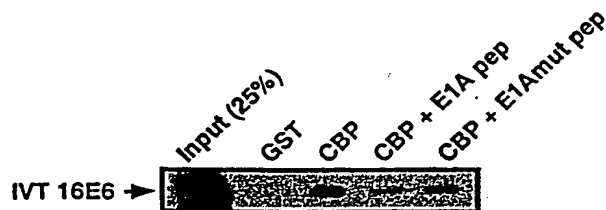
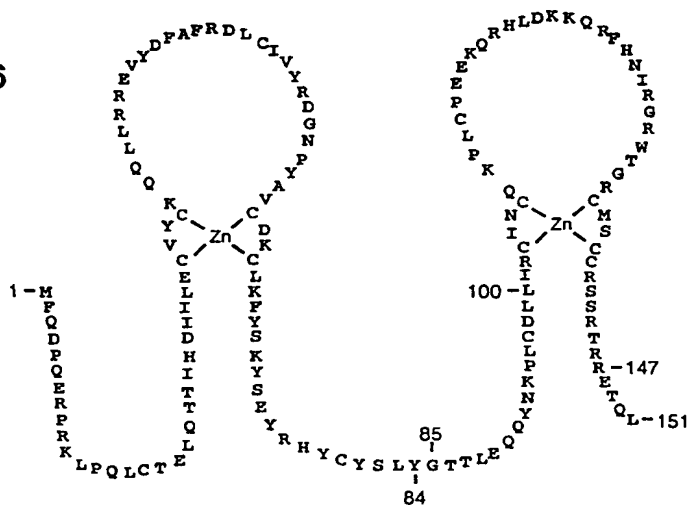


Figure 8

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A)

16 E6



B)

16 E6 constructs

CBP binding

1	151	+
1	147	+
1	84	-
85	151	+
100	147	+

C)

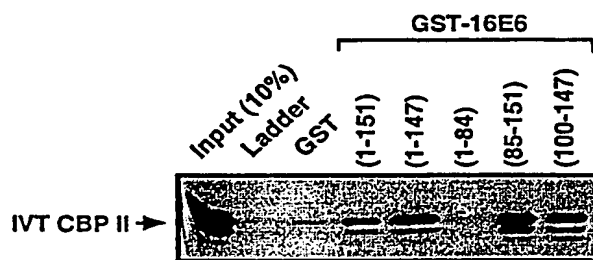
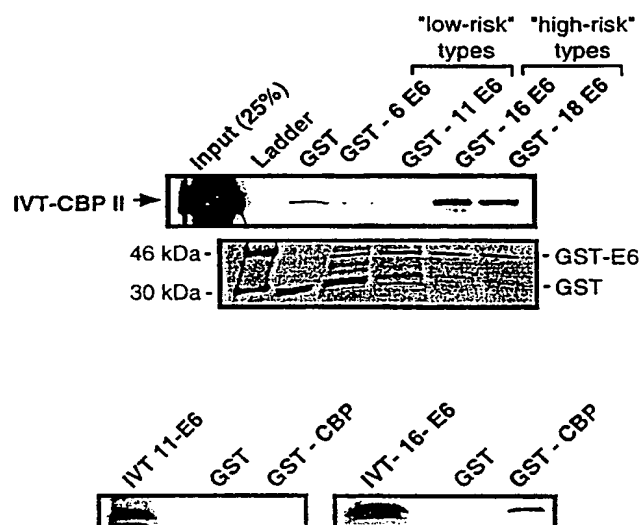


Figure 9

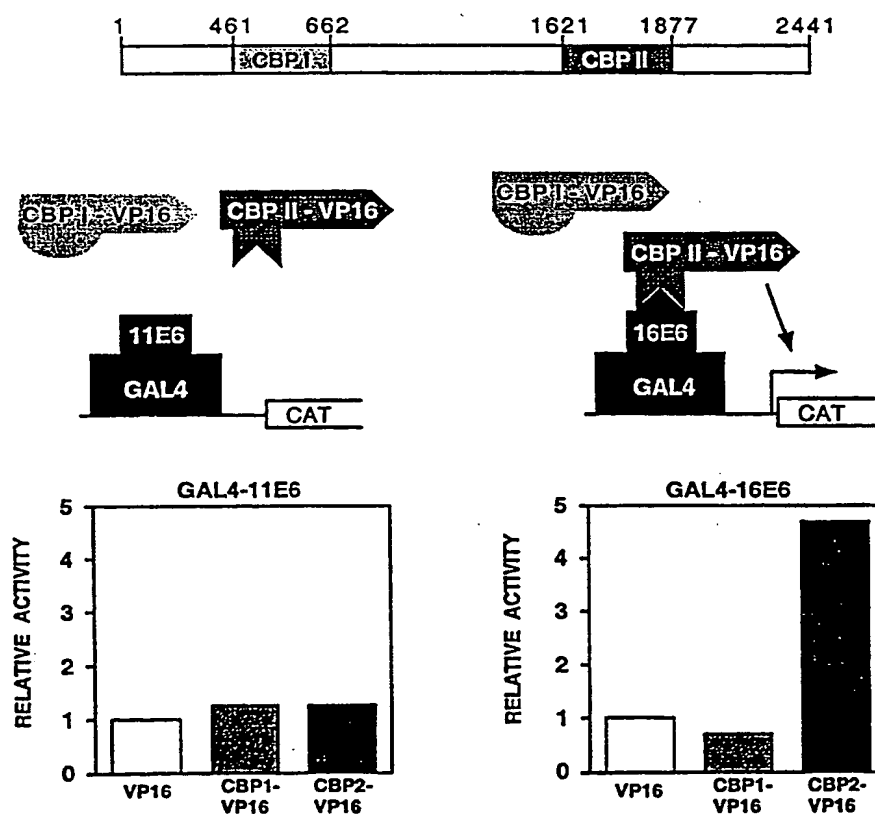
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Figure 10

A)



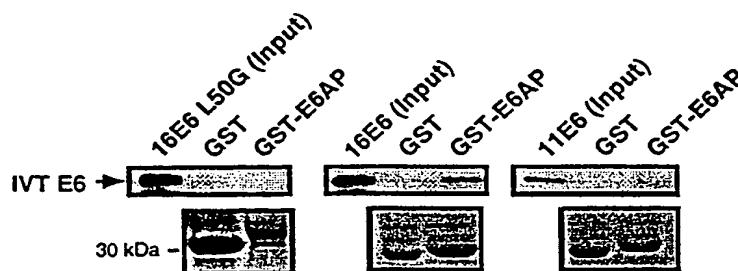
B)



A)



B)



C)

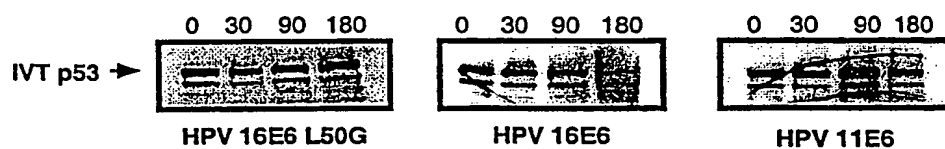
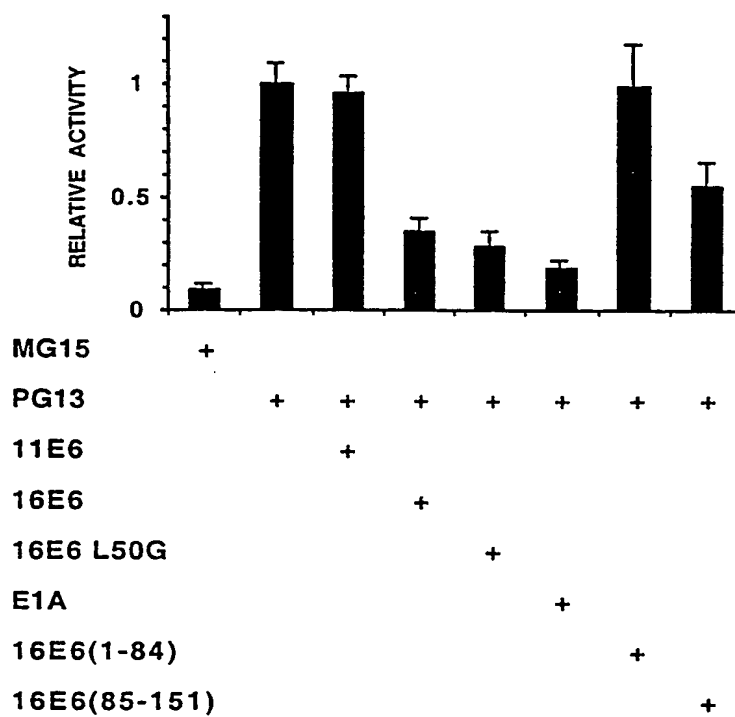


Figure 11

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A)



B)

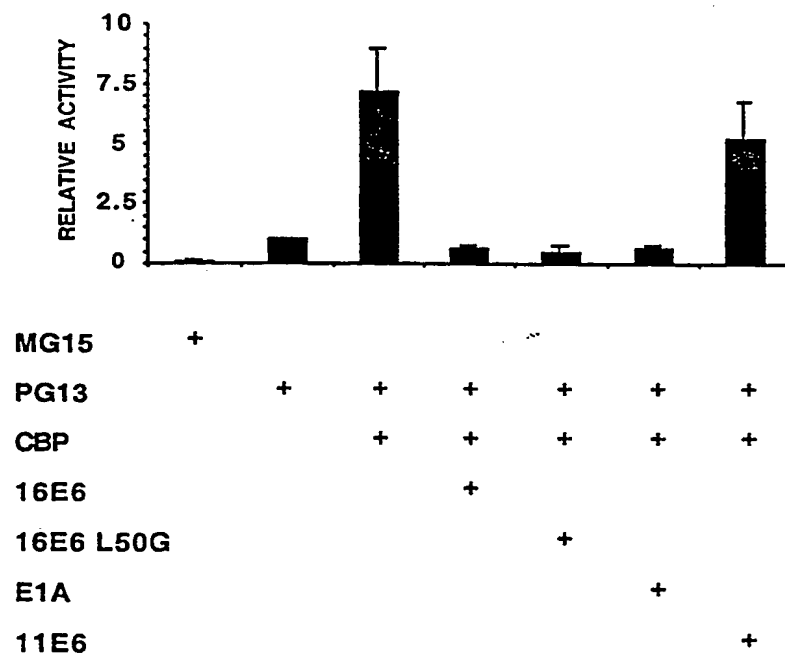


Figure 12

G	S	V	D	L	E	P	G	V	Q	K	L	x	x	x	gct	t	3'
gGA	TCC	CTC	GAC	CTC	GAG	CCC	GGG	CTG	CAG	AAG	CTT	GAT	TGA	TTa	gct	t	3'
cct	agG	CAG	CTG	GAG	CTC	GGG	CCC	GAC	CTC	TTC	GAA	CTA	ACT	AAT	GGA	a	5'
BamH1		Sall		Xho1		Sma1		Pst1		HindIII		stop (x3)			[core HindIII]		

Figure 13